

49  
50. (New) The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 90% sequence identity to SEQ ID NO: 22.

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51. (New) The promoter of claim 1, wherein the promoter comprises the nucleic acid sequence shown in SEQ ID NO: 22.

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52. (New) The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 80% sequence identity to SEQ ID NO: 17.

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53. (New) The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 90% sequence identity to SEQ ID NO: 17.

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54. (New) The promoter of claim 1, wherein the promoter comprises the nucleic acid sequence shown in SEQ ID NO: 17.

### Remarks

#### ***Restriction Requirement***

SEQ ID NOS: 17 and 22-25 should be examined in the same application, because SEQ ID NOS: 22-25 are sub-sequences of SEQ ID NO: 17 (see page 4, lines 8-21 and FIG. 3 of the present application), and are therefore related. Therefore, SEQ ID NOS 17 and 22-25, which were categorized into claim Groups I-V, respectively, should be examined in the same application.

Reconsideration of the restriction requirement is requested. Groups I-V (directed to a recombinant promoter, a vector, a host cell, a transgene, a plant cell, and a method of expressing a protein) and Group VI (claims 17-18 directed to a protein expressed using the method of claim 15) are inherently interconnected. In order to perform a thorough search of the prior art relevant to the claims of Groups I-V, the prior art relevant to claims 17 and 18 of Group VI also will have to be searched, as claims 17 and 18 depend from the claims of Groups I-V. Therefore, there is no additional burden on the Examiner to search both groups of claims. In the absence of

any burden on the Patent and Trademark Office, Groups I-V and Group VI should be examined in the same application.

In addition, Groups I-V (directed to a recombinant promoter, a vector, a host cell, a transgene, a plant cell, and a method of expressing a protein) and Group VII (claims 22-29, directed to a recombinant promoter including different promoter elements) are inherently interconnected. In order to perform a thorough search of the prior art relevant to the claims of Groups VII, the prior art relevant to Groups I-V also will have to be searched, as SEQ ID NO: 17 includes the promoter elements listed in claim 22. Therefore, there is no additional burden on the Examiner to search both groups of claims. In the absence of any burden on the Patent and Trademark Office, Groups I-V and Group VII should be examined in the same application.

#### ***Amendment***

By this Amendment, claims 2-6 are cancelled, and claims 30-54 are added. Therefore, claims 1 and 7-54 are now pending.

The specification was amended on page 4, lines 14-26. Specifically, the list of SEQ ID NOS: was corrected to reflect that SEQ ID NOS: 22-25, not 23-26, are fragments of SEQ ID NO: 17. Support for this amendment can be found in original claim 1, page 33, lines 10-16, FIG. 3, and in the sequence listing.

Claims 2-6 were cancelled, and re-written as claims 54, 51, 48 and 45, respectively, to more clearly show the relationship between the SEQ ID NOS.

Claim 1 was amended, and claims 34-54 added, to clarify the relationship between SEQ ID NOS: 17 and 22-25.

Claims 7-12, 14, 16, and 26-28 were amended for form, such as to correct antecedent basis and remove unnecessary punctuation.

Claim 15 was amended to remove an unnecessary step in the claim.

Claims 30-54 were added. Support for these new claims can be found throughout the specification, for example:

Claims 30-33: Claim 14, and page 5, lines 6-14;

Claims 34-54: Page 9, lines 13-21; and page 15, lines 21-25;

Claims 36-42: Page 10, lines 1-6.

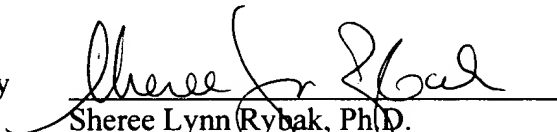
Therefore, no new matter is added by these amendments.

No amendment was made in response to prior art, nor was any amendment made to narrow the scope of any claim.

If there are any questions, the Examiner is invited to telephone the undersigned at the telephone number listed below.

Respectfully submitted,

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**Marked-up Version of Amended Claims and Specification  
Pursuant to 37 C.F.R. §§ 1.121(b)-(c)**

**In the specification:** Replace the two paragraphs on page 4, lines 14-26, with the following:

Another aspect of the invention provides fragments and deletions of the promoter, such as those shown in SEQ ID NOS: 22, 23, 24, 25, 26,] and variants thereof. The variant promoters are characterized by their retention of at least 50% sequence identity with the disclosed promoter sequences (SEQ ID NOS: 17, 22, 23, 24, [25,] and [26] 25), or by their retention of at least 20, 30, 40, 50, or 60 consecutive nucleic acid residues of the disclosed promoter sequences (SEQ ID NOS: 17, 22, 23, 24, [25,] and [26] 25). In each case these promoters at least retain promoter activity and, in some cases, these promoters exhibit native dfMTP promoter activity.

It is also contemplated that promoters such as the CaMV35S promoter may be altered through the introduction of one or more sequences found in the dfMTP promoter. The resulting promoter is characterized by its retention of at least 20, 30, 40, 50, or 60 consecutive nucleic acid residues of the disclosed promoter sequences (SEQ ID NOS: 17, 22, 23, 24, [25,] and [26] 25).

**In the claims:**

1. (Amended) A recombinant promoter, capable of driving expression of a transgene operably linked to the promoter, wherein the promoter [comprising] comprises a nucleic acid sequence [selected from the group consisting of:

- (a) the nucleic acid sequences shown in SEQ ID NOS: 17, 22, 23, 24, and 25;
- (b) a nucleic acid sequence] that shares at least [50%] 80% sequence identity to SEQ ID NO: 25 [with any of the nucleic acid sequences of (a); and
- (c) a nucleic acid sequence that comprises at least 20 consecutive nucleic acid residues of any of the nucleic acid sequences of (a), wherein the promoter is capable of driving the expression of a transgene operably linked to the promoter].

2. (Cancel) [The recombinant promoter of claim 1, comprising the nucleic acid sequence shown in SEQ ID NO: 17.]

3. (Cancel) [The recombinant promoter of claim 1, comprising the nucleic acid sequence shown in SEQ ID NO: 22.]

4. (Cancel) [The recombinant promoter of claim 1, comprising the nucleic acid sequence shown in SEQ ID NO: 23.]

5. (Cancel) [The recombinant promoter of claim 1, comprising the nucleic acid sequence shown in SEQ ID NO: 24.]

6. (Cancel) [The recombinant promoter of claim 1, comprising the nucleic acid sequence shown in SEQ ID NO: 25.]

7. (Amended) A vector, comprising [a] the recombinant promoter [as recited in] of claim 1.

8. (Amended) A host cell, comprising [a] the vector [as recited in] of claim 7.

9. (Amended) A transgenic plant, comprising [a] the host cell [as recited in] of claim 8.

10. (Amended) A transgene, comprising [a] the promoter [as recited in] of claim 1 and at least one ORF operably linked to the promoter.

11. (Amended) A vector, comprising [a] the transgene [as recited in] of claim 10.

12. (Amended) A plant cell, comprising [a] the transgene [as recited in] of claim 10.

14. (Amended) The plant cell of claim 12, wherein the plant cell is obtained from a plant selected from the group consisting of maize, wheat, rice, millet, tobacco, sorghum, rye, barley, brassica, sunflower, seaweeds, lemna, oat, soybean, cotton, legumes, rape/canola, alfalfa, flax, sunflower, safflower, brassica, cotton, flax, peanut, and clover; lettuce, tomato, cucurbits, cassava, potato, carrot, radish, pea, lentil, cabbage, cauliflower, broccoli, Brussel sprouts,

peppers, [and] other vegetables[;], citrus, apples, pears, peaches, apricots, walnuts, [and] other fruit trees[;], orchids, carnations, roses, [and] other flowers[;], cacao; poplar, elms, [and] other deciduous trees[;], pine, Douglas-fir, spruce, [and] other conifers[;], turf grasses[;], cacao[;], [and] rubber trees and [other] members of the genus *Hevea*.

15. (Amended) A method for expressing at least one protein in a host cell, comprising:  
[providing a transgene, comprising an ORF and a recombinant promoter as recited in claim 1;]

introducing [the] a transgene comprising an ORF and the recombinant promoter of claim 1 into a host cell; and

allowing the host cell to produce a protein from the ORF.

16. (Amended) The method [according] of claim 15, wherein the host cell is a plant host cell.

26. (Amended) A host cell, comprising [a] the vector [as recited in] of claim 25.

27. (Amended) A transgenic plant, comprising [a] the vector [as recited in] of claim 25.

28. (Amended) The transgenic plant of claim 27, wherein the transgenic plant is selected from the group consisting of maize, wheat, rice, millet, tobacco, sorghum, rye, barley, brassica, sunflower, seaweeds, lemna, oat, soybean, cotton, legumes, rape/canola, alfalfa, flax, sunflower, safflower, brassica, cotton, flax, peanut, and clover; lettuce, tomato, cucurbits, cassava, potato, carrot, radish, pea, lentil, cabbage, cauliflower, broccoli, Brussel sprouts, peppers, [and] other vegetables[;], citrus, apples, pears, peaches, apricots, walnuts, [and] other fruit trees[;], orchids, carnations, roses, [and] other flowers[;], cacao; poplar, elms, [and] other deciduous trees[;], pine, Douglas-fir, spruce, [and] other conifers[;], turf grasses[;], cacao[;], [and] rubber trees and [other] members of the genus *Hevea*.

30. (New) The plant cell of claim 14, wherein the plant cell is obtained from a tobacco plant.

31. (New) The plant cell of claim 14, wherein the plant cell is obtained from a potato plant.

32. (New) The plant cell of claim 14, wherein the plant cell is obtained from a wheat plant.

33. (New) The plant cell of claim 14, wherein the plant cell is obtained from a Douglas-fir plant.

34. (New) The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 90% sequence identity to SEQ ID NO: 25.

35. (New) The promoter of claim 1, wherein the promoter comprises the nucleic acid sequence shown in SEQ ID NO: 25.

36. (New) The promoter of claim 1, wherein the promoter comprises at least 20 consecutive nucleic acid residues of a nucleic acid sequence sharing at least 80% sequence identity to SEQ ID NO: 25.

37. (New) The promoter of claim 1, wherein the promoter comprises at least 20 consecutive nucleic acid residues of the nucleic acid sequence shown in SEQ ID NO: 25.

39. (New) The promoter of claim 1, wherein the promoter comprises at least 40 consecutive nucleic acid residues of a nucleic acid sequence sharing at least 90% sequence identity to SEQ ID NO: 25.

40. (New) The promoter of claim 1, wherein the promoter comprises at least 40 consecutive nucleic acid residues of the nucleic acid sequence shown in SEQ ID NO: 25.

41. (New) The promoter of claim 1, wherein the promoter comprises at least 60 consecutive nucleic acid residues of a nucleic acid sequence sharing at least 90% sequence identity to SEQ ID NO: 25.

42. (New) The promoter of claim 1, wherein the promoter comprises at least 60 consecutive nucleic acid residues of the nucleic acid sequence shown in SEQ ID NO: 25.

43. (New) The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 80% sequence identity to SEQ ID NO: 24.

44. (New) The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 90% sequence identity to SEQ ID NO: 24.

45. (New) The promoter of claim 1, wherein the promoter comprises the nucleic acid sequence shown in SEQ ID NO: 24.

46. (New) The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 80% sequence identity to SEQ ID NO: 23.

47. (New) The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 90% sequence identity to SEQ ID NO: 23.

48. (New) The promoter of claim 1, wherein the promoter comprises the nucleic acid sequence shown in SEQ ID NO: 23.

49. (New) The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 80% sequence identity to SEQ ID NO: 22.

50. (New) The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 90% sequence identity to SEQ ID NO: 22.



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52. (New) The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 80% sequence identity to SEQ ID NO: 17.

53. (New) The promoter of claim 1, wherein the promoter comprises a nucleic acid sequence sharing at least 90% sequence identity to SEQ ID NO: 17.

54. (New) The promoter of claim 1, wherein the promoter comprises the nucleic acid sequence shown in SEQ ID NO: 17.